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(54) Title: α-AMYLASE MUTANTS

(57) Abstract

The invention relates to a variant of a parent Termamyl-like α-amylase, comprising mutations in two, three, four, five or six regions/positions. The variants have increased thermostability at acidic pH and/or at low Ca^{2+} concentrations (relative to the parent). The invention also relates to a DNA construct comprising a DNA sequence encoding an α-amylase variant of the invention, a recombinant expression vector which carries a DNA construct of the invention, a cell which is transformed with a DNA construct of the invention, the use of an α-amylase variant of the invention for washing and/or dishwashing, textile desizing, starch liquefaction, a detergent additive comprising an α-amylase variant of the invention, a manual or automatic dishwashing detergent composition comprising an α-amylase variant of the invention, a method for generating a variant of a parent Termamyl-like α-amylase, which variant exhibits increased thermostability at acidic pH and/or at low Ca^{2+} concentrations (relative to the parent).

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Title: α-amylase mutants

FIELD OF THE INVENTION

The present invention relates, *inter alia*, to novel variants (mutants) of parent Termamyl-like α-amylases, notably variants exhibiting increased thermostability at acidic pH and/or at low Ca^{2+} concentrations (relative to the parent) which are advantageous with respect to applications of the variants in, industrial starch processing particularly (*e.g.* starch liquefaction or saccharification).

BACKGROUND OF THE INVENTION

α-Amylases (α-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) constitute a group of enzymes which catalyze hydrolysis of starch and other linear and branched 1,4-glucosidic oligo- and polysaccharides.

There is a very extensive body of patent and scientific literature relating to this industrially very important class of enzymes. A number of α-amylase such as Termamyl-like α-amylases variants are known from *e.g.* WO 90/11352, WO 95/10603, WO 95/26397, WO 96/23873 and WO 96/23874.

Among more recent disclosures relating to α-amylases, WO 96/23874 provides three-dimensional, X-ray crystal structural data for a Termamyl-like α-amylase which consists of the 300 N-terminal amino acid residues of the *B. amyloliquefaciens* α-amylase and amino acids 301-483 of the C-terminal end of the *B. licheniformis* α-amylase comprising the amino acid sequence (the latter being available commercially under the tradename Termamyl™), and which is thus closely related to the industrially important *Bacillus* α-amylases (which in the present context are embraced within the meaning of the term "Termamyl-like α-amylases", and which include, *inter alia*, the *B. licheniformis*, *B. amyloliquefaciens* and *B. stearothermophilus* α-amylases). WO 96/23874 further describes methodology for

designing, on the basis of an analysis of the structure of a parent Termamyl-like α-amylase, variants of the parent Termamyl-like α-amylase which exhibit altered properties relative to the parent.

WO 95/35382 (Gist Brocades B.V.) concerns amylolytic enzymes derived from *B. licheniformis* with improved properties allowing reduction of the Ca^{2+} concentration under application without a loss of performance of the enzyme. The amylolytic enzyme comprises one or more amino acid changes at positions selected from the group of 104, 128, 187, 188 of the *B. licheniformis* α-amylase sequence.

WO 96/23873 (Novo Nordisk) discloses Termamyl-like α-amylase variants which have increased thermostability obtained by pairwise deletion in the region R181*, G182*, T183* and G184* of the sequence shown in SEQ ID NO: 1 herein.

BRIEF DISCLOSURE OF THE INVENTION

The present invention relates to novel α-amylolytic variants (mutants) of a Termamyl-like α-amylase, in particular variants exhibiting increased thermostability (relative to the parent) which are advantageous in connection with the industrial processing of starch (starch liquefaction, saccharification and the like).

The inventors have surprisingly found out that in case of combining two, three, four, five or six mutations (will be described below), the thermostability of Termamyl-like α-amylases is increased at acidic pH and/or at low Ca^{2+} concentration in comparison to single mutations, such as the mutation dislcosed in WO 96/23873 (Novo Nordisk), *i.e.* pairwise deletion in the region R181*, G182*, T183* and G184* of the sequence shown in SEQ ID NO: 1 herein.

The invention further relates to DNA constructs encoding variants of the invention, to composition comprising variants of the invention, to methods for preparing variants of the invention, and to the use of variants and compositions of the invention, alone or in combination with other α-amylolytic

enzymes, in various industrial processes, *e.g.*, starch liquefaction.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 is an alignment of the amino acid sequences of six parent Termamyl-like α-amylases in the context of the invention. The numbers on the Extreme left designate the respective amino acid sequences as follows:

1: SEQ ID NO: 2,
2: Kaoamyl,
3: SEQ ID NO: 1,
4: SEQ ID NO: 5,
5: SEQ ID NO: 4,
6: SEQ ID NO: 3.

DETAILED DISCLOSURE OF THE INVENTION

<u>The Termamyl-like α-amylase</u>

It is well known that a number of α-amylases produced by *Bacillus* spp. are highly homologous on the amino acid level. For instance, the *B. licheniformis* α-amylase comprising the amino acid sequence shown in SEQ ID NO: 4 (commercially available as Termamyl™) has been found to be about 89% homologous with the *B. amyloliquefaciens* α-amylase comprising the amino acid sequence shown in SEQ ID NO: 5 and about 79% homologous with the *B. stearothermophilus* α-amylase comprising the amino acid sequence shown in SEQ ID NO: 3. Further homologous α-amylases include an α-amylase derived from a strain of the *Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513 or DSM 9375, all of which are described in detail in WO 95/26397, and the α-amylase described by Tsukamoto et al., Biochemical and Biophysical Research Communications, 151 (1988), pp. 25-31.

Still further homologous α-amylases include the α-amylase produced by the *B. licheniformis* strain described in EP 0252666 (ATCC 27811), and the α-amylases identified in WO 91/00353 and

WO 94/18314. Other commercial Termamyl-like *B. licheniformis* α-amylases are Optitherm™ and Takatherm™ (available from Solvay), Maxamyl™ (available from Gist-brocades/Genencor), Spezym AA™ and Spezyme Delta AA™ (available from Genencor), and Keistase™ (available from Daiwa).

Because of the substantial homology found between these α-amylases, they are considered to belong to the same class of α-amylases, namely the class of "Termamyl-like α-amylases".

Accordingly, in the present context, the term "Termamyl-like α-amylase" is intended to indicate an α-amylase which, at the amino acid level, exhibits a substantial homology to Termamyl™, i.e. the *B. licheniformis* α-amylase having the amino acid sequence shown in SEQ ID NO: 4 herein. In other words, a Termamyl-like α-amylase is an α-amylase which has the amino acid sequence shown in SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7 or 8 herein, and the amino acid sequence shown in SEQ ID NO: 1 of WO 95/26397 (the same as the amino acid sequence shown as SEQ ID NO: 7 herein) or in SEQ ID NO: 2 of WO 95/26397 (the same as the amino acid sequence shown as SEQ ID NO: 8 herein) or in Tsukamoto et al., 1988, (which amino acid sequence is shown in SEQ ID NO: 6 herein) or i) which displays at least 60%, preferred at least 70%, more preferred at least 75%, even more preferred at least 80%, especially at least 85%, especially preferred at least 90%, even especially more preferred at least 95% homology with at least one of said amino acid sequences shown in SEQ ID NOS 1 or 2 or 3 or 4 or 5 or 6 or 7 or 8 and/or ii) displays immunological cross-reactivity with an antibody raised against at least one of said α-amylases, and/or iii) is encoded by a DNA sequence which hybridizes to the DNA sequences encoding the above-specified α-amylases which are apparent from SEQ ID NOS: 9, 10, 11, or 12 of the present application (which encoding sequences encode the amino acid sequences shown in SEQ ID NOS: 1, 2, 3, 4 and 5 herein, respectively), from SEQ ID NO: 4 of WO 95/26397 (which DNA sequence, together with the stop codon TAA,

is shown in SEQ ID NO: 13 herein and encodes the amino acid sequence shown in SEQ ID NO: 8 herein) and from SEQ ID NO: 5 of WO 95/26397 (shown in SEQ ID NO: 14 herein), respectively.

In connection with property i), the "homology" may be determined by use of any conventional algorithm, preferably by use of the GAP progamme from the GCG package version 7.3 (June 1993) using default values for GAP penalties, which is a GAP creation penalty of 3.0 and GAP extension penalty of 0.1, (Genetic Computer Group (1991) Programme Manual for the GCG Package, version 7, 575 Science Drive, Madison, Wisconsin, USA 53711).

A structural alignment between Termamyl and a Termamyl-like α-amylase may be used to identify equivalent/corresponding positions in other Termamyl-like α-amylases. One method of obtaining said structural alignment is to use the Pile Up programme from the GCG package using default values of gap penalties, i.e., a gap creation penalty of 3.0 and gap extension penalty of 0.1. Other structural alignment methods include the hydrophobic cluster analysis (Gaboriaud et al., (1987), FEBS LETTERS 224, pp. 149-155) and reverse threading (Huber, T ; Torda, AE, PROTEIN SCIENCE Vol. 7, No. 1 pp. 142-149 (1998).

Property ii) of the α-amylase, i.e. the immunological cross reactivity, may be assayed using an antibody raised against, or reactive with, at least one epitope of the relevant Termamyl-like α-amylase. The antibody, which may either be monoclonal or polyclonal, may be produced by methods known in the art, *e.g.* as described by Hudson et al., Practical Immunology, Third edition (1989), Blackwell Scientific Publications. The immunological cross-reactivity may be determined using assays known in the art, examples of which are Western Blotting or radial immunodiffusion assay, *e.g.* as described by Hudson et al., 1989. In this respect, immunological cross-reactivity between the α-amylases having the amino acid sequences SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, or 8 respectively, have been found.

The oligonucleotide probe used in the characterization of the Termamyl-like α-amylase in accordance with property iii) above

may suitably be prepared on the basis of the full or partial nucleotide or amino acid sequence of the α-amylase in question.

Suitable conditions for testing hybridization involve presoaking in 5xSSC and prehybridizing for 1 hour at ~40°C in a solution of 20% formamide, 5xDenhardt's solution, 50mM sodium phosphate, pH 6.8, and 50mg of denatured sonicated calf thymus DNA, followed by hybridization in the same solution supplemented with 100mM ATP for 18 hours at ~40°C, followed by three times washing of the filter in 2xSSC, 0.2% SDS at 40°C for 30 minutes (low stringency), preferred at 50°C (medium stringency), more preferably at 65°C (high stringency), even more preferably at ~75°C (very high stringency). More details about the hybridization method can be found in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989.

In the present context, "derived from" is intended not only to indicate an α-amylase produced or producible by a strain of the organism in question, but also an α-amylase encoded by a DNA sequence isolated from such strain and produced in a host organism transformed with said DNA sequence. Finally, the term is intended to indicate an α-amylase which is encoded by a DNA sequence of synthetic and/or cDNA origin and which has the identifying characteristics of the α-amylase in question. The term is also intended to indicate that the parent α-amylase may be a variant of a naturally occurring α-amylase, i.e. a variant which is the result of a modification (insertion, substitution, deletion) of one or more amino acid residues of the naturally occurring α-amylase.

<u>Parent hybrid α-amylases</u>

The parent α-amylase may be a hybrid α-amylase, i.e. an α-amylase which comprises a combination of partial amino acid sequences derived from at least two α-amylases.

The parent hybrid α-amylase may be one which on the basis of amino acid homology and/or immunological cross-reactivity and/or

DNA hybridization (as defined above) can be determined to belong to the Termamyl-like α-amylase family. In this case, the hybrid α-amylase is typically composed of at least one part of a Termamyl-like α-amylase and part(s) of one or more other α-amylases selected from Termamyl-like α-amylases or non-Termamyl-like α-amylases of microbial (bacterial or fungal) and/or mammalian origin.

Thus, the parent hybrid α-amylase may comprise a combination of partial amino acid sequences deriving from at least two Termamyl-like α-amylases, or from at least one Termamyl-like and at least one non-Termamyl-like bacterial α-amylase, or from at least one Termamyl-like and at least one fungal α-amylase. The Termamyl-like α-amylase from which a partial amino acid sequence derives may, *e.g.*, be any of those specific Termamyl-like α-amylases referred to herein.

For instance, the parent α-amylase may comprise a C-terminal part of an α-amylase derived from a strain of *B. licheniformis*, and a N-terminal part of an α-amylase derived from a strain of *B. amyloliquefaciens* or from a strain of *B. stearothermophilus*. For instance, the parent α-amylase may comprise at least 430 amino acid residues of the C-terminal part of the *B. licheniformis* α-amylase, and may, *e.g.* comprise a) an amino acid segment corresponding to the 37 N-terminal amino acid residues of the *B. amyloliquefaciens* α-amylase having the amino acid sequence shown in SEQ ID NO: 5 and an amino acid segment corresponding to the 445 C-terminal amino acid residues of the *B. licheniformis* α-amylase having the amino acid sequence shown in SEQ ID No. 4, or b) an amino acid segment corresponding to the 68 N-terminal amino acid residues of the *B. stearothermophilus* α-amylase having the amino acid sequence shown in SEQ ID NO: 3 and an amino acid segment corresponding to the 415 C-terminal amino acid residues of the *B. licheniformis* α-amylase having the amino acid sequence shown in SEQ ID NO: 4.

The non-Termamyl-like α-amylase may, *e.g.*, be a fungal α-amylase, a mammalian or a plant α-amylase or a bacterial α-amylase (different from a Termamyl-like α-amylase). Specific examples of such α-amylases include the *Aspergillus oryzae* TAKA α-amylase, the *A. niger* acid α-amylase, the *Bacillus subtilis* α-amylase, the porcine pancreatic α-amylase and a barley α-amylase. All of these α-amylases have elucidated structures which are markedly different from the structure of a typical Termamyl-like α-amylase as referred to herein.

The fungal α-amylases mentioned above, i.e. derived from *A. niger* and *A. oryzae*, are highly homologous on the amino acid level and generally considered to belong to the same family of α-amylases. The fungal α-amylase derived from *Aspergillus oryzae* is commercially available under the tradename Fungamyl™.

Furthermore, when a particular variant of a Termamyl-like α-amylase (variant of the invention) is referred to - in a conventional manner - by reference to modification (*e.g.* deletion or substitution) of specific amino acid residues in the amino acid sequence of a specific Termamyl-like α-amylase, it is to be understood that variants of another Termamyl-like α-amylase modified in the equivalent position(s) (as determined from the best possible amino acid sequence alignment between the respective amino acid sequences) are encompassed thereby.

A preferred embodiment of a variant of the invention is one derived from a *B. licheniformis* α-amylase (as parent Termamyl-like α-amylase), e.g. one of those referred to above, such as the *B. licheniformis* α-amylase having the amino acid sequence shown in SEQ ID NO: 4.

Construction of variants of the invention

The construction of the variant of interest may be accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant. The variant may then

subsequently be recovered from the resulting culture broth. This is described in detail further below.

Altered properties of variants of the invention

The following discusses the relationship between mutations which may be present in variants of the invention, and desirable alterations in properties (relative to those a parent, Termamyl-like α-amylase) which may result therefrom.

Increased thermostability at acidic pH and/or at low Ca^{2+} concentration

Mutations of particular relevance in relation to obtaining variants according to the invention having increased thermostability at acidic pH and/or at low Ca^{2+} concentration include mutations at the following positions (relative to *B. licheniformis* α-amylase, SEQ ID NO: 4):

H156, N172, A181, N188, N190, H205, D207, A209, A210, E211, Q264, N265.

In the context of the invention the term "acidic pH" means a pH below 7.0, especially below the pH range, in which industrial starch liquefaction processes are normally performed, which is between pH 5.5 and 6.2.

In the context of the present invention the term "low Calcium concentration" means concentrations below the normal level used in industrial starch liquefaction. Normal concentrations vary depending of the concentration of free Ca^{2+} in the corn. Normally a dosage corresponding to 1mM (40ppm) is added which together with the level in corn gives between 40 and 60ppm free Ca^{2+} .

In the context of the invention the term "high tempertatures" means temperatures between 95°C and 160°C, especially the temperature range in which industrial starch liquefaction processes are normally performed, which is between 95°C and 105°C.

The inventors have now found that the thermostability at acidic pH and/or at low Ca^{2+} concentration may be increased even more by combining certain mutations including the above

mentioned mutations and/or I201 with each other.

Said "certain" mutations are the following (relative to *B. licheniformis* α-amylase, SEQ ID NO: 4):
N190, D207, E211, Q264 and I201.

Said mutation may further be combined with deletions in one, preferably two or even three positions as described in WO 96/23873 (*i.e.* in positions R181, G182, T183, G184 in SEQ ID NO: 1 herein). According to the invention variants of a parent Termamyl-like α-amylase with α-amylase activity comprising mutations in two, three, four, five or six of the above positions are contemplated.

It should be emphazised that not only the Termamyl-like α-amylases mentioned specifically below are contemplated. Also other commercial Termamyl-like α-amylases are contemplated. An unexhaustive list of such α-amylases is the following:
α-amylases produced by the *B. licheniformis* strain described in EP 0252666 (ATCC 27811), and the α-amylases identified in WO 91/00353 and WO 94/18314. Other commercial Termamyl-like *B. licheniformis* α-amylases are Optitherm™ and Takatherm™ (available from Solvay), Maxamyl™ (available from Gist-brocades/Genencor), Spezym AA™ Spezyme Delta AA™ (available from Genencor), and Keistase™ (available from Daiwa).

It may be mentioned here that amino acid residues, respectively, at positions corresponding to N190, I201, D207 and E211, respectively, in SEQ ID NO: 4 constitute amino acid residues which are conserved in numerous Termamyl-like α-amylases. Thus, for example, the corresponding positions of these residues in the amino acid sequences of a number of Termamyl-like α-amylases which have already been mentioned (*vide supra*) are as follows:

Table 1.

Termamyl-like α-amylase	N	I	D	E	Q

B. licheniformis (SEQ ID NO: 4)	N190	I201	D207	E211	Q264
B. amyloliquefaciens (SEQ ID NO: 5)	N190	V201	D207	E211	Q264
B. stearothermophilus (SEQ ID NO: 3)	N193	L204	E210	E214	---
Bacillus WO 95/26397 (SEQ ID NO: 2)	N195	V206	E212	E216	---
Bacillus WO 95/26397 (SEQ ID NO: 1)	N195	V206	E212	E216	---
"*Bacillus sp. #707*" (SEQ ID NO: 6)	N195	I206	E212	E216	---

Mutations of these conserved amino acid residues are very important in relation to improving thermostability at acidic pH and/or at low calcium concentration, and the following mutations are of particular interest in this connection (with reference to the numbering of the *B. licheniformis* amino acid sequence shown in SEQ ID NO: 4).

Pair-wise amino acid deletions at positions corresponding to R179-G182 in SEQ ID NO: 5 corresponding to a gap in Seq ID NO: 4. when aligned with a numerous Termamyl-like α-amylases. Thus, for example, the corresponding positions of these residues in the amino acid sequences of a number of Termamyl-like α-amylases which have already been mentioned (*vide supra*) are as follows:

Table 2.

Termamyl-like α-amylase	Pair wise amino acid deletions among
B. amyloliquefaciens (SEQ ID No.5)	R176, G177, E178, G179
B. stearothermophilus (SEQ ID No.3)	R179, G180, I181, G182
Bacillus WO 95/26397 (SEQ ID No.2)	R181, G182, T183, G184
Bacillus WO 95/26397 (SEQ ID No.1)	R181, G182, D183, G184
"*Bacillus sp. #707*" (SEQ ID No.6)	R181, G182, H183, G184

When using SEQ ID NO: 1 to SEQ ID NO: 6 as the backbone (i.e. as the parent Termamyl-like α-amylase) two, three, four, five or six mutations may according to the invention be made in the following regions/positions to increase the thermostability at acidic pH and/or at low Ca^{2+} concentrations (relative to the parent):

(relative to Seq ID NO: 1 herein):

1: R181*, G182*, T183*, G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 2 herein):
1: R181*,G182*,D183*,G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
(Relative to SEQ ID NO: 3 herein):
1: R179*,G180,I181*,G182*
2: N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
4: E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V
Relative to SEQ ID NO: 4 herein):
1: Q178*,G179*
2: N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: I201A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
4: D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 5 herein):
1: R176*,G177*,E178,G179*
2: N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
4: D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 6 herein):
1: R181*,G182*,H183*,G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;

3: I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V.

Comtemplated according to the present invention is combining three, four, five or six mutation.

Specific double mutations for backbone SEQ ID NO: 1 to SEQ ID NO: 6 are listed in the following.

Using SEQ ID NO: 1 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-R181*/G182*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/T183*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-T183*/G184*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-G182*/T183*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-T183*/G184*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-R181*/G182*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/T183*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-T183*/G184*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V:
-R181*/G182*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/T183*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-T183*/G184*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-G182*/T183*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-T183*/G184*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;

-V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;

Using SEQ ID NO: 2 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-R181*/G182*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/D183*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-D183*/G184*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-G182*/T183*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-T183*/G184*/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-R181*/G182*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/T183*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-T183*/G184*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/T183*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-T183*/G184*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-G182*/T183*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-T183*/G184*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-N195 A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-N195 A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V206 A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y

/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;

Using SEQ ID NO. 3 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-R179*/G180*/N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G180*/I181*/N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I181*/G182*/N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R179*/G180*/L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
-G180*/I181*/L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
-I181*/G182*/L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
-R179*/G180*/E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G180*/I181*/E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I181*/G182*/E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R179*/G180*/E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G180*/I181*/E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I181*/G182*/E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R179*/G180*/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-G180*/I181*/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-I181*/G182*/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
-N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V
/E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;

-L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V
/E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V
/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;
-E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V;

Using SEQ ID NO. 4 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-Q178*/G179*/N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-Q178*/G179*/I201A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
-Q178*/G179*/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-Q178*/G179*/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R179*/G180*/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190/I201A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
-N190/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I201/D207A,R,N,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I201/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I201/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-D207/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-D207/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E211/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;

Using SEQ ID NO: 5 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-R176*/G177*/N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G177*/E178*/N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E178*/G179*/N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R176*/G177*/V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-G176*/E178*/V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-E178*/G179*/V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;

-R176*/G177*/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G177*/E178*/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E178*/G179*/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R176*/G177*/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G177*/E178*/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E178*/G179*/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R176*/G177*/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G177*/E178*/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E178*/G179*/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
-N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y
/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

Using SEQ ID NO: 6 as the backbone the following double mutantions resulting in the desired effect are comtemplated according to the invention:

-R181*/G182*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/H183*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-H183*/G184*/N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
-G182*/H183*/I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;

-H183*/G184*/I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/H183*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-H183*/G184*/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-G182*/H183*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-H183*/G184*/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-R181*/G182*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-G182*/H183*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-H183*/G184*/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V
/E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
-E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
-E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V
/K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;

All Termamyl-like α-amylase defined above may suitably be used as backbone for preparing variants of the invention.

However, in a preferred embodiment the variant comprises the following mutations: N190F/Q264S in SEQ ID NO: 4 or in corresponding positiones in another parent Termamyl-like α-amylases.

In another embodiment the variant of the invention comprises

the following mutations: I181*/G182*/N193F in SEQ ID NO: 3 (TVB146) or in corresponding positions in another parent Termamyl-like α-amylases. Said variant may further comprise a substitution in position E214Q.

In a preferred embodiment of the invention the parent Termamyl-like α-amylase is a hybrid α-amylase of SEQ ID NO: 4 and SEQ ID NO: 5. Specifically, the parent hybrid Termamyl-like α-amylase may be a hybrid alpha-amylase comprising the 445 C-terminal amino acid residues of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4 and the 37 N-terminal amino acid residues of the α-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 5, which may suitably further have the following mutations: H156Y+A181T+N190F+A209V+Q264S (using the numbering in SEQ ID NO: 4). The latter mentioned hybrid is used in the examples below and is referred to as LE174.

General mutations in variants of the invention

It may be preferred that a variant of the invention comprises one or more modifications in addition to those outlined above. Thus, it may be advantageous that one or more proline residues present in the part of the α-amylase variant which is modified is/are replaced with a non-proline residue which may be any of the possible, naturally occurring non-proline residues, and which preferably is an alanine, glycine, serine, threonine, valine or leucine.

Analogously, it may be preferred that one or more cysteine residues present among the amino acid residues with which the parent α-amylase is modified is/are replaced with a non-cysteine residue such as serine, alanine, threonine, glycine, valine or leucine.

Furthermore, a variant of the invention may - either as the only modification or in combination with any of the above outlined modifications - be modified so that one or more Asp and/or Glu present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 4 is replaced by an Asn and/or Gln, respectively. Also of interest is the

replacement, in the Termamyl-like α-amylase, of one or more of the Lys residues present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 4 by an Arg.

It will be understood that the present invention encompasses variants incorporating two or more of the above outlined modifications.

Furthermore, it may be advantageous to introduce point-mutations in any of the variants described herein.

<u>Methods for preparing α-amylase variants</u>

Several methods for introducing mutations into genes are known in the art. After a brief discussion of the cloning of α-amylase-encoding DNA sequences, methods for generating mutations at specific sites within the α-amylase-encoding sequence will be discussed.

<u>Cloning a DNA sequence encoding an α-amylase</u>

The DNA sequence encoding a parent α-amylase may be isolated from any cell or microorganism producing the α-amylase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the α-amylase to be studied. Then, if the amino acid sequence of the α-amylase is known, homologous, labelled oligonucleotide probes may be synthesized and used to identify α-amylase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labelled oligonucleotide probe containing sequences homologous to a known α-amylase gene could be used as a probe to identify α-amylase-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying α-amylase-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming α-amylase-negative bacteria with the resulting genomic DNA library, and

then plating the transformed bacteria onto agar containing a substrate for α-amylase, thereby allowing clones expressing the α-amylase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g. the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers (1981) or the method described by Matthes et al. (1984). In the phosphoroamidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. (1988).

Site-directed mutagenesis

Once an α-amylase-encoding DNA sequence has been isolated, and desirable sites for mutation identified, mutations may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites; mutant nucleotides are inserted during oligonucleotide synthesis. In a specific method, a single-stranded gap of DNA, bridging the α-amylase-encoding sequence, is created in a vector carrying the α-amylase gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al. (1984). US 4,760,025 discloses the introduction of oligonucleotides encoding multiple

mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method, because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method for introducing mutations into α-amylase-encoding DNA sequences is described in Nelson and Long (1989). It involves the 3-step generation of a PCR fragment containing the desired mutation introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Random Mutagenesis

Random mutagenesis is suitably performed either as localised or region-specific random mutagenesis in at least three parts of the gene translating to the amino acid sequence shown in question, or within the whole gene.

The random mutagenesis of a DNA sequence encoding a parent α-amylase may be conveniently performed by use of any method known in the art.

In relation to the above, a further aspect of the present invention relates to a method for generating a variant of a parent α-amylase, e.g. wherein the variant exhibits altered or increased thermal stability relative to the parent, the method comprising:

(a) subjecting a DNA sequence encoding the parent α-amylase to random mutagenesis,
(b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and
(c) screening for host cells expressing anα-amylase variant which has an altered property (i.e. thermal stability) relative to the parent α-amylase.

Step (a) of the above method of the invention is preferably performed using doped primers.

For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the random mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, *e.g.*, be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) ir-radiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA sequence encoding the parent enzyme to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during the synthesis of the oligonucleotide at the positions which are to be changed. The doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide can be incorporated into the DNA encoding the α-amylase enzyme by any published technique, using *e.g.* PCR, LCR or any DNA polymerase and ligase as deemed appropriate.

Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and mutation in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, *e.g.*, so as to allow for the introduction of 90% wild type and 10% mutations in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program which, *inter alia*, ensures that introduction of stop codons is avoided.

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent α-amylase is subjected to PCR under conditions that increase the mis-incorporation of nucleotides (Deshler 1992; Leung et al., Technique, Vol.1, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., Molec. Gen. Genet., 133, 1974, pp. 179-191), *S. cereviseae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the α-amylase by, *e.g.*, transforming a plasmid containing the parent glycosylase into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may be conveniently present in a genomic or cDNA library prepared from an organism expressing the parent α-amylase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or other-wise exposed to the mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harboured in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA sequence prior to performing the expression step b) or the screening step c). Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the parent enzyme.

Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are the following: gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* or *Streptomyces murinus*; and gram-negative bacteria such as *E. coli*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

Localized random mutagenesis

The random mutagenesis may be advantageously localized to a part of the parent α-amylase in question. This may, *e.g.*, be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the parent enzyme has been elucidated and related to the function of the enzyme.

The localized, or region-specific, random mutagenesis is conveniently performed by use of PCR generated mutagenesis techniques as described above or any other suitable technique known in the art. Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, *e.g.*, by insertion into a suitable vector, and said part may be subsequently subjected to mutagenesis by use of any of the mutagenesis methods discussed above.

Alternative methods of providing α-amylase variants

Alternative methods for providing variants of the invention include gene shuffling method known in the art including the methods *e.g.* described in WO 95/22625 (from Affymax Technologies N.V.) and WO 96/00343 (from Novo Nordisk A/S).

Expression of α-amylase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an α-amylase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected

to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding an α-amylase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* α-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α-amylase, *A. niger* acid stable α-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to

hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g. when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α-amylases mentioned herein comprise a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding an α-amylase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of an α-amylase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, *e.g.* by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are grampositive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*,

Bacillus brevis, Bacillus stearothermophilus, Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus coagulans, Bacillus circulans, Bacillus lautus, Bacillus megaterium, Bacillus thuringiensis, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favourably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, *e.g.* *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In yet a further aspect, the present invention relates to a method of producing an α-amylase variant of the invention, which method comprises cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the α-amylase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (*e.g.* as described in catalogues of the American Type Culture Collection).

The α-amylase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Industrial applications

The α-amylase variants of this invention possesses valuable properties allowing for a variety of industrial applications. In particular, enzyme variants of the invention are applicable as a component in washing, dishwashing and hard-surface cleaning detergent compositions. Numerous variants are particularly useful in the production of sweeteners and ethanol from starch, and/or for textile desizing. Conditions for conventional starch-conversion processes, including starch liquefaction and/or saccharification processes, are described in, e.g., US 3,912,590 and in EP patent publications Nos. 252 730 and 63 909.

Production of sweeteners from starch:

A "traditional" process for conversion of starch to fructose syrups normally consists of three consecutive enzymatic processes, viz. a liquefaction process followed by a saccharification process and an isomerization process. During the liquefaction process, starch is degraded to dextrins by an α-amylase (*e.g.* Termamyl™) at pH values between 5.5 and 6.2 and at temperatures of 95-160°C for a period of approx. 2 hours. In order to ensure an optimal enzyme stability under these conditions, 1 mM of calcium is added (40 ppm free calcium ions).

After the liquefaction process the dextrins are converted into dextrose by addition of a glucoamylase (*e.g.* AMG™) and a debranching enzyme, such as an isoamylase or a pullulanase (*e.g.* Promozyme™). Before this step the pH is reduced to a value below 4.5, maintaining the high temperature (above 95°C), and the liquefying α-amylase activity is denatured. The temperature is lowered to 60°C, and glucoamylase and debranching enzyme are added. The saccharification process proceeds for 24-72 hours.

After the saccharification process the pH is increased to a value in the range of 6-8, preferably pH 7.5, and the calcium is removed by ion exchange. The dextrose syrup is then converted into high fructose syrup using, *e.g.*, an immmobilized glucoseisomerase (such as Sweetzyme™).

At least 1 enzymatic improvements of this process could be envisaged. Reduction of the calcium dependency of the liquefying α-amylase. Addition of free calcium is required to

ensure adequately high stability of the α-amylase, but free calcium strongly inhibits the activity of the glucoseisomerase and needs to be removed, by means of an expensive unit operation, to an extent which reduces the level of free calcium to below 3-5 ppm. Cost savings could be obtained if such an operation could be avoided and the liquefaction process could be performed without addition of free calcium ions.

To achieve that, a less calcium-dependent Termamyl-like α-amylase which is stable and highly active at low concentrations of free calcium (< 40 ppm) is required. Such a Termamyl-like α-amylase should have a pH optimum at a pH in the range of 4.5-6.5, preferably in the range of 4.5-5.5.

Detergent compositions

As mentioned above, variants of the invention may suitably be incorporated in detergent compositions. Increased thermostability at low calcium concentrations would be very beneficial for amylase performance in detergents, i.e. the alkaline region. Reference is made, for example, to WO 96/23874 and WO 97/07202 for further details concerning relevant ingredients of detergent compositions (such as laundry or dishwashing detergents), appropriate methods of formulating the variants in such detergent compositions, and for examples of relevant types of detergent compositions.

Detergent compositions comprising a variant of the invention may additionally comprise one or more other enzymes, such as a lipase, cutinase, protease, cellulase, peroxidase or laccase, and/or another α-amylase.

α-amylase variants of the invention may be incorporated in detergents at conventionally employed concentrations. It is at present contemplated that a variant of the invention may be incorporated in an amount corresponding to 0.00001-1 mg (calculated as pure, active enzyme protein) of α-amylase per liter of wash/dishwash liquor using conventional dosing levels of detergent.

The invention also relates to a composition comprising

a mixture of one or more variants of the invention derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3 and a Termamyl-like alpha-amylase derived from the *B. licheniformis* α-amylase having the sequence shown in SEQ ID NO: 4.

Further, the invention also relates to a composition comprising a mixture of one or more variants according the invention derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3 and a hybrid alpha-amylase comprising a part of the *B. amyloliquefaciens* α-amylase shown in SEQ ID NO: 5 and a part of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4. The latter mentioned hydrid Termamyl-like α-amylase comprises the 445 C-terminal amino acid residues of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4 and the 37 N-terminal amino acid residues of the α-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 5. Said latter mentioned hybrid α-amylase may suitably comprise the following mutations: H156Y+A181T+N190F+A209V+Q264S (using the numbering in SEQ ID NO: 4). In the examples below said hybrid parent Termamyl-like α-amylase, is used in combination with variants of the invention, which variants may be used in compositions of the invention.

In a specific embodiment of the invention the composition comprises a mixture of TVB146 and LE174, e.g., in a ratio of 2:1 to 1:2, such as 1:1.

A α-amylase variant of the invention or a composition of the invention may in an aspect of the invention be used for washing and/or dishwashing; for textile desizing or for starch liquefaction.

MATERIALS AND METHODS

Enzymes:

BSG alpha-amylase: *B. stearothermophilus* alpha-amylase depicted in SEQ ID NO: 3.

TVB146 alpha-amylase variant: *B. stearothermophilus* alpha-amylase variant depicted in SEQ ID NO: 3 with the following mutations: with the deletion in positions I181-G182 + N193F.

LE174 hybrid alpha-amylase variant:

LE174 is a hybrid Termamyl-like alpha-amylase being identical to the Termamyl sequence, i.e., the *Bacillus licheniformis* α-amylase shown in SEQ ID NO: 4, except that the N-terminal 35 amino acid residues (of the mature protein) has been replaced by the N-terminal 33 residues of BAN (mature protein), i.e., the *Bacillus amyloliquefaciens* alpha-amylase shown in SEQ ID NO: 5, which further havefollowing mutations: H156Y+A181T+N190F+A209V+Q264S (using the numbering in SEQ ID NO: 4). LE174 was constructed by SOE-PCR (Higuchi et al. 1988, Nucleic Acids Research 16:7351).

Fermentation and purification of α-amylase variants

A *B. subtilis* strain harbouring the relevant expression plasmid is streaked on a LB-agar plate with 10 µg/ml kanamycin from -80°C stock, and grown overnight at 37°C.

The colonies are transferred to 100 ml BPX media supplemented with 10 µg/ml kanamycin in a 500 ml shaking flask.

Composition of BPX medium:

Potato starch	100	g/l
Barley flour	50	g/l
BAN 5000 SKB	0.1	g/l
Sodium caseinate	10	g/l
Soy Bean Meal	20	g/l
Na_2HPO_4, 12 H_2O	9	g/l
Pluronic™	0.1	g/l

The culture is shaken at 37°C at 270 rpm for 5 days.

Cells and cell debris are removed from the fermentation broth by centrifugation at 4500 rpm in 20-25 minutes. Afterwards the supernatant is filtered to obtain a completely clear solution. The filtrate is concentrated and washed on a UF-filter (10000 cut off membrane) and the buffer is changed to 20mM Acetate pH 5.5. The UF-filtrate is applied on a S-sepharose F.F. and elution is carried out by step elution with 0.2M NaCl in the same buffer. The eluate is dialysed against 10mM Tris, pH 9.0 and applied on a Q-sepharose F.F. and eluted with a linear gradient from 0-0.3M NaCl over 6 column volumes. The fractions which contain the activity (measured by the Phadebas assay) are pooled, pH was adjusted to pH 7.5 and remaining color was removed by a treatment with 0.5% W/vol. active coal in 5 minutes.

Activity determination - (KNU)

One Kilo alpah-amylase Unit (1 KNU) is the amount of enzyme which breaks down 5.26 g starch (Merck, Amylum Solubile, Erg. B 6, Batch 9947275) per hour in Novo Nordisk's standard method for determination of alpha-amylase based upon the following condition:

Substrate	soluble starch
Calcium content in solvent	0.0043 M
Reaction time	7-20 minutes
Temperature	37°C
pH	5.6

Detailed description of Novo Nordisk's analytical method (AF 9) is available on request.

BS-amylase Activity Determination - KNU(S)

1. Application Field

This method is used to determine α-amylase activity in fermentation and recovery samples and formulated and granulated products.

2. Principle

BS-amylase breaks down the substrate (4,6-ethylidene(G_7)-p-nitrophenyl(G_1)-α,D-maltoheptaoside (written as ethylidene-G_7-PNP) into, among other things, G_2-PNP and G_3-PNP, where G denoted glucose and PNP p-nitrophenol.

G2-PNP and G3-PNP are broken down by α-glucosidase, which is added in excess, into glucose and the yellow-coloured p-nitrophenol.

The colour reaction is monitored in situ and the change in absorbance over time calculated as an expression of the spreed of the reaction and thus of the activity of the enzyme. See the Boehringer Mannheim 1442 309 guidelines for further details.

2.1 Reaction conditions

Reaction:

Temperature : 37°C

pH : 7.1

Pre-incubation time: 2 minutes

Detection:

Wavelength : 405 nm

Measurement time 3 minutes

3. Definition of Units

Bacillus stearothermophius alpha-amylase (BS-amylase) activity is determined relative to a standard of declared activity and stated in Kilo Novo Units (Stearothermophilus) or KNU(S)).

4. Specificity and Sensitivity

Limit of determination: approx. 0.4 KNU(s)/g

5. Apparatus

Cobas Fara analyser

Diluted (e.g. Hamilton Microlab 1000)

Analytical balance (e.g. Mettler AE 100)

Stirrer plates

6. Reagents/Substrates

A ready-made kit is used in this analysis to determine α-amylase activity. Note that the reagents specified for the substrate and α-glucosidase are not used as described in the Boehringer Mannheim guidelines. However, the designations "buffer", "glass 1", glass 1a" and Glass 2" are those referred to in those guidelines.

6.1. Substrate

4,6-ethylidene(G_7)-p-nitrophenyl(G_1)-α,D-maltoheptaoside (written as ethylidene-G_7-PNP) e.g. Boehringer Mannheim 1442 309

6.2 α-glucosidase help reagent

α-glucosidase, e.g. Boehringer Mannheim 1442 309

6.3 BRIJ 35 solution

BRIJ 35 (30% W/V Sigma 430 AG-6)	1000 mL
Demineralized water	up to 2,000 mL

6.4 Stabiliser

Brij 35 solution	33 mL
$CaCl_2$*$2H_2O$ (Merck 2382)	882 g
Demineralized water	up to 2,000 mL

7. Samples and Standards

7.1 Standard curve

Example: Preparation of BS-amylase standard curve

The relevant standard is diluted to 0.60 KNU(s)/mL as follows. A calculated quantity of standard is weighed out and added to 200 mL volumetric flask, which is filled to around the 2/3 mark with demineralized water. Stabiliser corresponding to 1% of the volume of the flask is added and the flask is filled to the mark with demineralized water.

A Hamilton Microlab 1000 is used to produce the dilutions shown below. Demineralized water with 1% stabiliser is used as the diluent.

Dilution No.	Enzyme stock solution	1% stabiliser	KNU(s)/mL
1	20μL	580μL	0.02
2	30μL	570μL	0.03
3	40μL	560μL	0.04
4	50μL	550μL	0.05
5	60μL	540μL	0.06

7.2 Level control

A Novo Nordisk A/S BS amylase level control is included in all runs using the Cobas Fara. The control is diluted with 1% stabiliser so that the final dilution is within the range of the standard curve. All weights and dilutions are noted on the worklist

7.3 Sample solutions

Single determination

Fermentation samples (not final samples) from production, all fermentation samples from pilot plants and storage stability samples are weighed out and analyzed once only.

Double determination over 1 run:

Process samples, final fermentation samples from production, samples from GLP studies and R&D samples are weighed out and analyzed twice.

Double determinations over 2 runs:

Finished product samples are weighed out and analyzed twice over two separate runs.

Maximum concentration of samples in powder form: 5%

Test samples are diluted with demineralized water with 1% stabiliser to approx. 0.037 KNU(S)/mL on the basis of their expected activity. The final dilution is made direct into the sample cup.

8. Procedure

8.1 Cobas Menu Program

- The Cobas Menu Program is used to suggest the weight/dilutions of samples and level control to be used.
- The samples are entered into the program with a unique identification code and a worklist is printed out
- The samples and control are weighed out and diluted as stated on the worklist with hand-written weight data is inserted into the BS-amylase analysis logbook
- The results are computered automatically by the Cobas Fara as described in item 9 and printed out along with the standard curve.
- Worklists and results printouts are inserted into the BS-amylase analysis logbook.

8.2 Cobas Fara set-up

- The samples are placed in the sample rack
- The five standards are placed in the calibration rack at position 1 to 5 (strongest standard at position 5), and control placed in the same rack at position 10.
- The substrate is transferred to a 30 mL reagent container and placed in that reagent rack at position 2 (holder 1).
- The α-glucosidase help reagent is transferred to a 50 mL reagent container and placed in the reagent rack at position 2 (holder C)

8.3 Cobas Fare analysis

The main principles of the analysis are as follows:

20µL sample and 10µL rinse-water are pipetted into the cuvette along with 250µL α-glucosidase help reagent. The cuvette rotates for 10 seconds and the reagents are thrown out into the horizontal cuvettes. 25µL substrate and 20µL rinse-water are pipetted off. After a 1 second wait to ensure that the temperature is 37°C, the cuvette rotates again and the substrate is mixed into the horizontal cuvettes. Absorbance is measured for the first time after 120 seconds and then every 5 seconds. Absorbance is measured a total of 37 times for each sample.

9. Calculations

The activity of the samples is calculated relative to Novo Nordisk A/S standard.

The standard curve is plotted by the analyzer. The curve is to be gently curved, rising steadily to an absorbance of around 0.25 for standard no. 5.

The activity of the samples in KNU(S)/mL is read off the standard curve by the analyzer.

The final calculations to allow for the weights/dilutions used employ the following formula:

Activity in KNU(S)/g = S x V X F/W

S= analysis result read off (KNU(S)/mL

V= volume of volumetric flask used in mL

F= dilution factor for second dilution

W= weight of enzyme sample in g

9.2 Calculation of mean values

Results are stated with 3 significant digits. However, for sample activity < 10 KNU(S)/g, only 2 significant digits are given.

The following rules apply on calculation of mean values:

1. Data which deviates more than 2 standard deviations from the mean value is not included in the calculation.

2. Single and double determination over one run:

The mean value is calculated on basis of results lying within the standard curve's activity area.

3. Double determinations over two runs: All values are included in the mean value. Outliers are omitted.

10. Accuracy and Precision

The coefficient of variation is 2.9% based on retrospective validation of analysis results for a number of finished products and the level control.

Assay for α-Amylase Activity

α-Amylase activity is determined by a method employing Phadebas® tablets as substrate. Phadebas tablets (Phadebas® Amylase Test, supplied by Pharmacia Diagnostic) contain a cross-linked insoluble blue-coloured starch polymer which has been mixed with bovine serum albumin and a buffer substance and tabletted.

For every single measurement one tablet is suspended in a tube containing 5 ml 50 mM Britton-Robinson buffer (50 mM acetic acid, 50 mM phosphoric acid, 50 mM boric acid, 0.1 mM $CaCl_2$, pH adjusted to the value of interest with NaOH). The test is performed in a water bath at the temperature of interest. The α-amylase to be tested is diluted in x ml of 50 mM Britton-Robinson buffer. 1 ml of this α-amylase solution is added to the 5 ml 50 mM Britton-Robinson buffer. The starch is hydrolysed by the α-amylase giving soluble blue fragments. The absorbance of the resulting blue solution, measured spectrophotometrically at 620 nm, is a function of the α-amylase activity.

It is important that the measured 620 nm absorbance after 10 or 15 minutes of incubation (testing time) is in the range of 0.2 to 2.0 absorbance units at 620 nm. In this absorbance range there is linearity between activity and absorbance (Lambert-Beer law). The dilution of the enzyme must therefore be adjusted to fit this criterion. Under a specified set of conditions (temp., pH, reaction time, buffer conditions) 1 mg of a given α-amylase will hydrolyse a certain amount of substrate and a blue colour will be produced. The colour intensity is measured at 620 nm. The measured absorbance is directly proportional to the specific

activity (activity/mg of pure α-amylase protein) of the α-amylase in question under the given set of conditions.

EXAMPLES

EXAMPLE 1

Construction of variants of BSG α-amylase (SEQ ID NO: 3)

The gene encoding BSG, amyS, is located in plasmid pPL1117. This plasmid contains also the gene conferring resistance towards kanamycin and an origin of replication, both obtained from plasmid pUB110 (Gryczan, T.J. et al (1978) J.Bact 134:318-329).

The DNA sequence of the mature part of amyS is shown as SEQ ID NO: 11 and the amino acid sequence of the mature protein is shown as SEQ ID NO: 3

BSG variant TVB145, which contains a deletion of 6 nucleotides corresponding to amino acids I181-G182 in the mature protein, is constructed as follows:

Polymerase Chain Reaction (PCR) is utilized to amplify the part of the amyS gene (from plasmid pPL1117), located between DNA primers BSG1 (SEQ ID NO: 15) and BSGM2 (SEQ ID NO: 18). BSG1 is identical to a part of the amyS gene whereas BSGM2 contains the 6 bp nucleotide deletion. A standard PCR reaction is carried out: 94°C for 5 minutes, 25 cycles of (94°C for 45 seconds, 50°C for 45 seconds, 72°C for 90 seconds), 72°C for 7 minutes using the Pwo polymerase under conditions as recommended by the manufacturer, Boehringer Mannheim Gmbh.

The resulting approximately 550 bp amplified band was used as a megaprimer (Barik, S and Galinski, MS (1991): Biotechniques 10: 489-490) together with primer BSG3 in a second PCR with pPL1117 as template resulting in a DNA fragment of approximately 1080 bp.

This DNA fragment is digested with restriction endonucleases Acc65I and SalI and the resulting approximately 550 bp fragment is ligated into plasmid pPL1117 digested with the same enzymes and transformed into the protease- and amylase-deleted *Bacillus subtilis* strain SHA273 (described in WO92/11357 and WO95/10603).

Kanamycin resistant and starch degrading transformants were analysed for the presence of the desired mutations (restriction

digest to verify the introduction of a HindIII site in the gene). The DNA sequence between restriction sites Acc65I and SalI was verified by DNA sequencing to ensure the presence of only the desired mutations.

BSG variant TVB146 which contains the same 6 nucleotide deletion as TVB145 and an additional substitution of asparagine 193 for a phenylalanine, N193F, was constructed in a similar way as TVB145 utilizing primer BSGM3 (SEQ ID NO: 19) in the first PCR.

BSG variant TVB161, containing the deletion of I181-G182, N193F, and L204F, is constructed in a similar way as the two previous variants except that the template for the PCR reactions is plasmid pTVB146 (pPL1117 containing the TVB146-mutations within amyS and the mutagenic oligonucleotide for the first PCR is BSGM3.

BSG variant TVB162, containing the deletion of I181-G182, N193F, and E210H, is constructed in a similar way as TVB161 except that the mutagenic oligonucleotide is BSGM4 (SEQ ID NO: 20).

BSG variant TVB163, containing the deletion of I181-G182, N193F, and E214Q, is constructed in a similar way as TVB161 except that the mutagenic oligonucleotide is BSGM5 (SEQ ID NO: 21).

The above constructed BSG variants were then fermented and purified as described above in the "Material and Methods" section.

EXAMPLE 2

Measurement of the calcium- and pH-dependent stability

Normally, the industrial liquefaction process runs using pH 6.0-6.2 as liquefaction pH and an addition of 40 ppm free calcium in order to improve the stability at 95°C-105°C. Some of the herein proposed substitutions have been made in order to improve the stability at

1. lower pH than pH 6.2 and/or
2. at free calcium levels lower than 40 ppm free calcium.

Two different methods have been used to measure the improvements in stability obtained by the different

substitutions in the α-amylase from *B.stearothermophilus*:

Method 1. One assay which measures the stability at reduced pH, pH 5.0, in the presence of 5 ppm free calcium.

10 μg of the variant were incubated under the following conditions: A 0.1 M acetate solution, pH adjusted to pH 5.0, containing 5ppm calcium and 5% w/w common corn starch (free of calcium). Incubation was made in a water bath at 95°C for 30 minutes.

Method 2. One assay which measure the stability in the absence of free calcium and where the pH is maintained at pH 6.0. This assay measures the decrease in calcium sensitivity:

10 μg of the variant were incubated under the following conditions: A 0.1 M acetate solution, pH adjusted to pH 6.0, containing 5% w/w common corn starch (free of calcium). Incubation was made in a water bath at 95°C for 30 minutes.

Stability determination

All the stability trials 1, 2 have been made using the same set up. The method was:

The enzyme was incubated under the relevant conditions (1-4). Samples were taken at 0, 5, 10, 15 and 30 minutes and diluted 25 times (same dilution for all taken samples) in assay buffer (0.1M 50mM Britton buffer pH 7.3) and the activity was measured using the Phadebas assay (Pharmacia) under standard conditions pH 7.3, 37°C.

The activity measured before incubation (0 minutes) was used as reference (100%). The decline in percent was calculated as a function of the incubation time. The table shows the residual activity after 30 minutes of incubation.

Stability method 1. / Low pH stability improvement

MINUTES OF INCUBATION	WT. SEQ. ID. NO:3 AMYLASE (BSG)	SEQ. ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 (TVB145)	SEQ. ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 + N193F (TVB146)	SEQ. ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 + N193F + E214Q (TVB163)
0	100	100	100	100
5	29	71	83	77
10	9	62	77	70
15	3	50	72	67
30	1	33	62	60

Stability method 1. / Low pH stability improvement
The temperature describet in method 1 has been reduced from 95°C to 70°C since the amylases mentioned for SEQ ID NO: 1 and 2 have a lower thermostability than the one for SEQ ID NO: 3.

MINUTES OF INCUBATION	WT. SEQ. ID. NO: 2 AMYLASE	SEQ. ID NO: 2 VARIANT WITH DELETION IN POS. D183-G184	SEQ. ID NO: 1 AMYLASE	SEQ. ID NO: 1 VARIANT WITH DELETION IN POS. T183-G184
0	100	100	100	100
5	73	92	41	76
10	59	88	19	69
15	48	91	11	62
30	28	92	3	59

Stability method 2. / Low calcium sensitivity

MINUTES OF INCUBATION	WT. SEQ ID NO: 3 AMYLASE (BSG)	SEQ ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 (TVB145)	SEQ ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 + N193F (TVB146)	SEQ ID NO: 3 VARIANT WITH DELETION IN POS. I181-G182 + N193F + E214Q (TVB163)
0	100	100	100	100
5	60	82	81	82
10	42	76	80	83
15	31	77	81	79
30	15	67	78	79

Specific activity determination.

The specific activity was determined using the Phadebas assay (Pharmacia) as activity/mg enzyme. The activity was determined using the α-amylase assay described in the Materials and Methods section herein.

The specific activity of the parent enzyme and a single and a double mutation was determined to:

BSG: SEQ ID NO:3 (Parent enzyme) 20000 NU/mg

TVB145: SEQ ID NO:3 with the deletion in positions I181-G182: (Single mutation) 34600 NU/mg

TVB146: SEQ ID NO:3 with the deletion in positions I181-G182 + N193F: (Double mutation) 36600 NU/mg

TVB163: SEQ ID NO:3 with the deletion in positions I181-G182+N193F+E214Q: (Triple mutation) 36300 NU/mg

EXAMPLE 3

Pilot plant jet cook and liquefaction with alpha-amylase

variant TVB146

Pilot plant liquefaction experiments were run in the mini-jet system using a dosage of 50 NU (S)/g DS at pH 5.5 with 5 ppm added Ca^{++}, to compare the performance of formulated BSG alpha-amylase variant TVB146 (SEQ ID NO: 3 with deletion in positions
I181-G182 + N193F) with that of parent BSG alpha-amylase (SEQ ID NO: 3). The reaction was monitored by measuring the DE increase (Neocuproine method) as a function of time.

Corn starch slurries were prepared by suspending 11.8 kg Cerestar C*Pharm GL 03406 (89 % starch) in deionized water and making up to 30 kg. The pH was adjusted to 5.5 at ambient temperature, after the addition of 0.55 g $CaCl_2 \cdot 2H_2O$.

The following enzymes were used:

TVB146	108 KNU(S)/g, 146 KNU(SM9)/g
BSG amylase	101 KNU(S)/g, 98 KNU(SM9)/g

An amount of enzyme corresponding to 50 NU (SM9)/g DS was added, and the conductivity adjusted to 300mS using NaCl. The standard conditions were as follows:

Substrate concentration	35 % w/w (initial)
	31.6-31.9 % w/w (final)
Temperature	105°C, 5 min (Primary liquefaction)
	95°C, 90 min (Secondary liquefaction)
pH (initial)	5.5

After jetting, the liquefied starch was collected and transported in sealed thermos-flasks from the pilot plant to the laboratory, where secondary liquefaction was continued at 95 °C.

10 ml samples were taken at 15 minute intervals from 15-90 minutes. 2 drops of 1 N HCl were added to inactivate the enzyme. From these samples, 0.3-0.1 g (according to the expected DE) were weighed out and diluted to 100 ml. Reducing sugars were then determined according to the Neocuproine method (Determination of reducing sugar with improved precision.

Dygert, Li, Florida and Thomas (1965). Anal. Biochem 13, 368) and DE values determined. The development of DE as a function of time is given in the following table:

	TVB146	BSG
Time (min.)	DE (neocuproine)	
15	2.80	2.32
30	4.88	3.56
45	6.58	4.98
60	8.17	6.00
75	9.91	7.40
90	11.23	8.03

As can be seen the alpha-amylase variant TVB146 performed significantly better under industrially relevant application conditions at low levels of calcium than the parent BSG alpha-amylase.

EXAMPLE 4

Jet Cook and Liquefaction with a combination of alpha-amylase variants (TVB146 and LE174)

Jet cook and liquefaction using a combination of the alpha-amylase variants, TVB146 and LE174 (ratio 1:1) were carried out at the following conditions:

Substrate A.E. Staley food grade powdered corn starch (100lbs)

D.S. 35% using DI water

Free Ca^{2+} 2.7ppm at pH 5.3 (none added, from the starch only)

Initial pH 5.3

Dose AF9 units (AF9 is available on request) for each enzyme variant was 28 NU/g starch db for a total dose of 56 NU/g

Temperature in primary liquefaction 105°C

Hold time in primary liquefaction 5 minutes

Temperature in secondary liquefaction 95°C

At 15 minutes into secondary liquefaction 1.5 gms of hydrolyzate was added to a tared one liter volumetric containing 500cc of DI water and 1 ml of one normal HCl and the exact wt. added was recorded. This was repeated at 15 minute intervals out to 90 minutes with an additional point at 127

minutes. These were diluted to one liter and determined for dextrose equivalence via Neocuproine method as discribed by Dygert,Li, Florida and Thomas. Determination of reducing sugar with improved precision (1965). Anal. Biochem 13, 368.

The results were as follows:

Time	DE
15	3.2
30	4.8
45	6.3
60	7.8
75	9.4
90	10.4
127	13.1

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CLAIMS

1. A variant of a parent Termamyl-like α-amylase with α-amylase activity comprising mutations in two, three, four, five or six of the following regions/positions or in corresponding positions in other parent Termamyl-like α-amylases:

(relative to SEQ ID NO: 1):
1: R181*, G182*, T183*, G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 2):
1: R181*,G182*,D183*,G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V206A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;
(Relative to SEQ ID NO: 3):
1: R179*,G180,I181*,G182*
2: N193A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: L204A,R,D,N,C,E,Q,G,H,I,K,M,F,P,S,T,W,Y,V;
4: E210A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E214A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: S267A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,T,W,Y,V
Relative to SEQ ID NO: 4):
1: N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
2: I201A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
3: D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
4: E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 5):
1: R176*,G177*,E178,G179*
2: N190A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: V201A,R,D,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y;

4: D207A,R,N,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E211A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: Q264A,R,D,N,C,E,G,H,I,L,K,M,F,P,S,T,W,Y,V;
(relative to SEQ ID NO: 6):
1: R181*,G182*,H183*,G184*
2: N195A,R,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
3: I206A,R,D,N,C,E,Q,G,H,L,K,M,F,P,S,T,W,Y,V;
4: E212A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
5: E216A,R,D,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V;
6: K269A,R,D,N,C,E,Q,G,H,I,L,M,F,P,S,T,W,Y,V;

2. The variant according to claim 1, comprising the following mutations: N190F/Q264S in SEQ ID NO: 4 or in corresponding positions in another parent α-amylase.

3. The variant according to claim 1, comprising the following mutations: I181*/G182*/N193F in SEQ ID NO: 3 or in corresponding positions in another parent Termamyl like α-amylase.

4. The variant according to claim 3, further comprising a substitution in position E214Q in SEQ ID NO: 3 or in a corresponding position in another parent Termamyl like α-amylase.

5. The variant according to any of claims 1 to 4, wherein the parent α-amylase is a hybrid α-amylase of SEQ ID NO: 4 and SEQ ID NO: 5.

6. The variant according to claim 5, wherein the parent hybrid α-amylase is a hybrid alpha-amylase comprising the 445 C-terminal amino acid residues of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4 and the 37 N-terminal amino acid residues of the α-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 5.

7. The variant according to claim 6, wherein the parent hybrid

Termamyl-like α-amylase further has the following mutations: H156Y+A181T+N190F+A209V+Q264S (using the numbering in SEQ ID NO: 4).

8. The variant according to claim 1, exhibiting increased stability at acidic pH and/or low Ca^{2+} concentration:

9. A DNA construct comprising a DNA sequence encoding an α-amylase variant according to any one of claims 1 to 8.

10. A recombinant expression vector which carries a DNA construct according to claim 9.

11. A cell which is transformed with a DNA construct according to claim 9 or a vector according to claim 10.

12. A cell according to claim 11, which is a microorganism.

13. A cell according to claim 12, which is a bacterium or a fungus.

14. The cell according to claim 13, which is a grampositive bacterium such as *Bacillus subtilis, Bacillus licheniformis, Bacillus lentus, Bacillus brevis, Bacillus stearothermophilus, Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus coagulans, Bacillus circulans, Bacillus lautus* or *Bacillus thuringiensis*.

15. A detergent additive comprising an α-amylase variant according to any one of claims 1 to 8, optionally in the form of a non-dusting granulate, stabilised liquid or protected enzyme.

16. A detergent additive according to claim 15 which contains 0.02-200 mg of enzyme protein/g of the additive.

17. A detergent additive according to claims 15 or 16, which additionally comprises another enzyme such as a protease, a

lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

18. A detergent composition comprising an α-amylase variant according to any of claims 1 to 8.

19. The detergent composition according to claim 18 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

20. A manual or automatic dishwashing detergent composition comprising an α-amylase variant according to any one of claims 1 to 8.

21. A dishwashing detergent composition according to claim 20 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

22. A manual or automatic laundry washing composition comprising an α-amylase variant according to any one of claims 1 to 8.

23. A laundry washing composition according to claim 22, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, an amylolytic enzyme and/or a cellulase.

24. A composition comprising:

(i) a mixture of the α-amylase from *B. licheniformis* having the sequence shown in SEQ ID NO: 4 with one or more variants according to any of claims 1 to 8 derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3; or

(ii) a mixture of the α-amylase from *B. stearothermophilus* having the sequence shown in SEQ ID NO: 3 with one or more variants according to any of claims 1 to 8 derived from one or more other parent Termamyl-like α-amylases; or

(iii) a mixture of one or more variants according any of claim 1 to 8 derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3 with one or more variants according to the invention derived from one or more other parent Termamyl-like α-amylases.

25. A composition comprising:
a mixture of one or more variants according any of claims 1 to 8 derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3 and a Termamyl-like alpha-amylase derived from the *B. licheniformis* α-amylase having the sequence shown in SEQ ID NO: 4.

26. The composition comprising:
a mixture of one or more variants according any of claims 1 to 8 derived from (as the parent Termamyl-like α-amylase) the *B. stearothermophilus* α-amylase having the sequence shown in SEQ ID NO: 3 and a hybrid alpha-amylase comprising a part of the *B. amyloliquefaciens* α-amylase shown in SEQ ID NO: 5 and a part of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4.

27. The composition according to claim 26, wherein the hybrid α-amylase is a hybrid alpha-amylase comprising the 445 C-terminal amino acid residues of the *B. licheniformis* α-amylase shown in SEQ ID NO: 4 and the 37 N-terminal amino acid residues of the α-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 5.

28. The composition according to claim 27, wherein the hybrid α-amylase further has the following mutations:
H156Y+A181T+N190F+A209V+Q264S (using the numbering in SEQ ID NO: 4).

29. The composition according to claims 26, comprising a mixture

of TVB146 and LE174.

30. Use of an α-amylase variant according to any of claims 1 to 8 or a composition according to any of claims 24 to 29 for washing and/or dishwashing.

31. Use of an α-amylase variant according to any of claims 1 to 8 or a composition according to any of claims 24 to 29 for textile desizing.

32. Use of an α-amylase variant according to any of claims 1 to 8 or a composition according to any of claims 24 to 29 for starch liquefaction.

33. A method for generating a variant of a parent Termamyl-like α-amylase, which variant exhibits increased stability at low pH and at low calcium concentration relative to the parent, the method comprising:

(a) subjecting a DNA sequence encoding the parent Termamyl-like α-amylase to random mutagenesis,

(b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and

(c) screening for host cells expressing a mutated α-amylase which has increased stability at low pH and low calcium concentration relative to the parent α-amylase.

```
    1                                                  50
1   HHNGTNGTMM QYFEWHLPND GNHWNRLRDD ASNLRNRGIT AIWIPPAWKG
2   ..NGTNGTMM QYFEWYLPND GNHWNRLRSD ASNLKDKGIS AVWIPPAWKG
3   HHNGTNGTMM QYFEWYLPND GNHWNRLRDD AANLKSKGIT AVWIPPAWKG
4   ....VNGTLM QYFEWYTPND GQHWKRLQND AEHLSDIGIT AVWIPPAYKG
5   ..ANLNGTLM QYFEWYMPND GQHWRRLQND SAYLAEHGIT AVWIPPAYKG
6   .AAPFNGTMM QYFEWYLPDD GTLWTKVANE ANNLSSLGIT ALWLPPAYKG

    51                                                100
1   TSQNDVGYGA YDLYDLGEFN QKGTVRTKYG TRSQLESAIH ALKNNGVQVY
2   ASQNDVGYGA YDLYDLGEFN QKGTIRTKYG TRNQLQAAVN ALKSNGIQVY
3   TSQNDVGYGA YDLYDLGEFN QKGTVRTKYG TRNQLQAAVT SLKNNGIQVY
4   LSQSDNGYGP YDLYDLGEFQ QKGTVRTKYG TKSELQDAIG SLHSRNVQVY
5   TSQADVGYGA YDLYDLGEFH QKGTVRTKYG TKGELQSAIK SLHSRDINVY
6   TSRSDVGYGV YDLYDLGEFN QKGTVRTKYG TKAQYLQAIQ AAHAAGMQVY

    101                                               150
1   GDVVMNHKGG ADATENVLAV EVNPNNRNQE ISGDYTIEAW TKFDFPGRGN
2   GDVVMNHKGG ADATEMVRAV EVNPNNRNQE VSGEYTIEAW TKFDFPGRGN
3   GDVVMNHKGG ADGTEIVNAV EVNRSNRNQE TSGEYAIEAW TKFDFPGRGN
4   GDVVLNHKAG ADATEDVTAV EVNPANRNQE TSEEYQIKAW TDFRFPGRGN
5   GDVVINHKGG ADATEDVTAV EVDPADRNRV ISGEHLIKAW THFHFPGRGS
6   ADVVFDHKGG ADGTEWVDAV EVNPSDRNQE ISGTYQIQAW TKFDFPGRGN

    151                                               200
1   TYSDFKWRWY HFDGVDWDQS RQFQNRIYKF RGDGKAWDWE VDSENGNYDY
2   THSNFKWRWY HFDGVDWDQS RKLNNRIYKF RGDGKGWDWE VDTENGNYDY
3   NHSSFKWRWY HFDGTDWDQS RQLQNKIYKF RGTGKAWDWE VDTENGNYDY
4   TYSDFKWHWY HFDGADWDES RKI.SRIFKF RGEGKAWDWE VSSENGNYDY
5   TYSDFKWHWY HFDGTDWDES RKL.NRIYKF ..QGKAWDWE VSNENGNYDY
6   TYSSFKWRWY HFDGVDWDES RKL.SRIYKF RGIGKAWDWE VDTENGNYDY
```

Fig. 1

```
     201                                                        250
1    LMYADVDMDH PEVVNELRRW GEWYTNTLNL DGFRIDAVKH IKYSFTRDWL
2    LMYADIDMDH PEVVNELRNW GVWYTNTLGL DGFRIDAVKH IKYSFTRDWS
3    LMYADVDMDH PEVIHELRNW GVWYTNTLNL DGFRIDAVKH IKYSFTRDWL
4    LMYADVDYDH PDVVAETKKW GIWYANELSL DGFRIDAAKH IKFSFLRDWV
5    LMYADIDYDH PDVAAEIKRW GTWYANELQL DGFRLDAVKH IKFSFLRDWV
6    LMYADLDMDH PEVVTELKNW GKWYVNTTNI DGFRLDAVKH IKFSFFPDWL

     251                                                        300
1    THVRNATGKE MFAVAEFWKN DLGALENYLN KTNWNHSVFD VPLHYNLYNA
2    IHVRSATGKN MFAVAEFWKN DLGAIENYLN KTNWNHSVFD VPLHYNFYNA
3    THVRNTTGKP MFAVAEFWKN DLGAIENYLN KTSWNHSAFD VPLHYNLYNA
4    QAVRQATGKE MFTVAEYWQN NAGKLENYLN KTSFNQSVFD VPLHFNLQAA
5    NHVREKTGKE MFTVAEYWQN DLGALENYLN KTNFNHSVFD VPLHYQFHAA
6    SYVRSQTGKP LFTVGEYWSY DINKLHNYIT KTDGTMSLFD APLHNKFYTA

     301                                                        350
1    SNSGGNYDMA KLLNGTVVQK HPMHAVTFVD NHDSQPGESL ESFVQEWFKP
2    SKSGGNYDMR QIFNGTVVQR HPMHAVTFVD NHDSQPEEAL ESFVEEWFKP
3    SNSGGYYDMR NILNGSVVQK HPTHAVTFVD NHDSQPGEAL ESFVQQWFKP
4    SSQGGGYDMR RLLDGTVVSR HPEKAVTFVE NHDTQPGQSL ESTVQTWFKP
5    STQGGGYDMR KLLNGTVVSK HPLKSVTFVD NHDTQPGQSL ESTVQTWFKP
6    SKSGGAFDMR TLMTNTLMKD QPTLAVTFVD NHDTEPGQAL QSWVDPWFKP

     351                                                        400
1    LAYALILTRE QGYPSVFYGD YYGIPTHS.. .VPAMKAKID PILEARQNFA
2    LAYALTLTRE QGYPSVFYGD YYGIPTHG.. .VPAMKSKID PILEARQKYA
3    LAYALVLTRE QGYPSVFYGD YYGIPTHG.. .VPAMKSKID PLLQARQTFA
4    LAYAFILTRE SGYPQVFYGD MYGTKGTSPK EIPSLKDNIE PILKARKEYA
5    LAYAFILTRE SGYPQVFYGD MYGTKGDSQR EIPALKHKIE PILKARKQYA
6    LAYAFILTRQ EGYPCVFYGD YYGIPQYN.. .IPSLKSKID PLLIARRDYA
```

Figure 1 (continued)

Fig. 1

```
     401                                                   450
  1  YGTQHDYFDH HNIIGWTREG NTTHPNSGLA TIMSDGPGGE KWMYVGQNKA
  2  YGRQN..... .......... .......... .......... ..........
  3  YGTQHDYFDH HDIIGWTREG NSSHPNSGLA TIMSDGPGGN KWMYVGKNKA
  4  YGPQHDYIDH PDVIGWTREG DSSAAKSGLA ALITDGPGGS KRMYAGLKNA
  5  YGAQHDYFDH HDIVGWTREG DSSVANSGLA ALITDGPGGA KRMYVGRQNA
  6  YGTQHDYLDH SDIIGWTREG GTEKPGSGLA ALITDGPGGS KWMYVGKQHA

     451                                                   500
  1  GQVWHDITGN KPGTVTINAD GWANFSVNGG SVSIWVKR.. ..........
  2  .......... .......... .......... .......... ..........
  3  GQVWRDITGN RTGTVTINAD GWGNFSVNGG SVSVWVKQ.. ..........
  4  GETWYDITGN RSDTVKIGSD GWGEFHVNDG SVSIYVQ... ..........
  5  GETWHDITGN RSEPVVINSE GWGEFHVNGG SVSIYVQR.. ..........
  6  GKVFYDLTGN RSDTVTINSD GWGEFKVNGG SVSVWVPRKT TVSTIARPIT

     501              519
  1  .......... .........
  2  .......... .........
  3  .......... .........
  4  .......... .........
  5  .......... .........
  6  TRPWTGEFVR WTEPRLVAW
```

Figure 1 (continued)

Fig. 1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: NOVO NORDISK A/S
(B) STREET: Novo Alle
(C) CITY: DK-2880 Bagsvaerd
(E) COUNTRY: Denmark
(F) POSTAL CODE (ZIP): DK-2880
(G) TELEPHONE: +45 44 44 88 88
(H) TELEFAX: +45 44 49 32 56

(ii) TITLE OF INVENTION: AMYLASE VARIANTS

(iii) NUMBER OF SEQUENCES: 21

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1               5                   10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
            20                  25                  30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
        35                  40                  45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65                  70                  75                  80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
                85                  90                  95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
        115                 120                 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140
```

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly

435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Lys Arg
485

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
1 5 10 15

Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
20 25 30

Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
35 40 45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
50 55 60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
195 200 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys

225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
485 490 495

Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
500 505 510

Ala Trp

(2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1               5                   10                  15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
            20                  25                  30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
        35                  40                  45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
    50                  55                  60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65                  70                  75                  80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
                85                  90                  95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
            100                 105                 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
        115                 120                 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
    130                 135                 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145                 150                 155                 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
                165                 170                 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
        195                 200                 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
    210                 215                 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240
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Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
                245                     250                     255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
            260                     265                     270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
        275                     280                     285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
    290                     295                     300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305                     310                     315                     320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                     330                     335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                     345                     350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                     360                     365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
    370                     375                     380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385                     390                     395                     400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
                405                     410                     415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                     425                     430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
        435                     440                     445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                     455                     460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                     470                     475                     480

Val Gln Arg
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1               5                   10                  15

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
        35                  40                  45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
    50                  55                  60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65                  70                  75                  80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
    130                 135                 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
        195                 200                 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
    210                 215                 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245                 250                 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
            260                 265                 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
        275                 280                 285
```

```
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
    290                 295                 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                 330                 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                 375                 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                 390                 395                 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                 440                 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450                 455                 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                 470                 475                 480
```

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1               5                   10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
            20                  25                  30
```

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro

```
                325                 330                 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
            340                 345                 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
    370                 375                 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385                 390                 395                 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
        435                 440                 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
    450                 455                 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

Ile Trp Val Asn Lys
                485
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1               5                   10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
            20                  25                  30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
        35                  40                  45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65                  70                  75                  80
```

```
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
                 85                  90                  95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
        115                 120                 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145                 150                 155                 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
                165                 170                 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
        195                 200                 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
    210                 215                 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225                 230                 235                 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
                245                 250                 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
            260                 265                 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
        275                 280                 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
    290                 295                 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305                 310                 315                 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325                 330                 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
            340                 345                 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365
```

```
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
    370                 375                 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385                 390                 395                 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
        435                 440                 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
    450                 455                 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

Val Trp Val Lys Gln
                485
```

(2) INFORMATION FOR SEQ ID NO: 8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1               5                   10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
            20                  25                  30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
        35                  40                  45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65                  70                  75                  80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
                85                  90                  95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
```

115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

```
Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
        435                 440                 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
    450                 455                 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

Ile Trp Val Lys Arg
                485
```

(2) INFORMATION FOR SEQ ID NO: 9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
CATCATAATG GAACAAATGG TACTATGATG CAATATTTCG AATGGTATTT GCCAAATGAC      60

GGGAATCATT GGAACAGGTT GAGGGATGAC GCAGCTAACT TAAAGAGTAA AGGGATAACA     120

GCTGTATGGA TCCCACCTGC ATGGAAGGGG ACTTCCCAGA ATGATGTAGG TTATGGAGCC     180

TATGATTTAT ATGATCTTGG AGAGTTTAAC CAGAAGGGGA CGGTTCGTAC AAAATATGGA     240

ACACGCAACC AGCTACAGGC TGCGGTGACC TCTTTAAAAA ATAACGGCAT TCAGGTATAT     300

GGTGATGTCG TCATGAATCA TAAAGGTGGA GCAGATGGTA CGGAAATTGT AAATGCGGTA     360

GAAGTGAATC GGAGCAACCG AAACCAGGAA ACCTCAGGAG AGTATGCAAT AGAAGCGTGG     420

ACAAAGTTTG ATTTTCCTGG AAGAGGAAAT AACCATTCCA GCTTTAAGTG GCGCTGGTAT     480

CATTTTGATG GGACAGATTG GGATCAGTCA CGCCAGCTTC AAAACAAAAT ATATAAATTC     540

AGGGGAACAG GCAAGGCCTG GGACTGGGAA GTCGATACAG AGAATGGCAA CTATGACTAT     600

CTTATGTATG CAGACGTGGA TATGGATCAC CCAGAAGTAA TACATGAACT TAGAAACTGG     660

GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT     720

ATAAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA     780

ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT     840

AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA     900
```

TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA 960

CATCCAACAC ATGCCGTTAC TTTTGTTGAT AACCATGATT CTCAGCCCGG GGAAGCATTG 1020

GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA 1080

CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCCG 1140

GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACTTTTGC CTATGGTACG 1200

CAGCATGATT ACTTTGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC 1260

CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG 1320

TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC 1380

ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG 1440

GTTTGGGTGA AGCAA 1455

(2) INFORMATION FOR SEQ ID NO: 10:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT 60

GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC 120

GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAAA ATGATGTGGG GTATGGAGCC 180

TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTCGTAC TAAGTATGGG 240

ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT 300

GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC 360

GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG 420

ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT 480

CATTTCGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC 540

CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT 600

TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG 660

GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT 720

ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GAAACGCAAC GGGAAAAGAA 780

ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT 840

AAAACAAACT GGAATCATTC TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG 900

TCAAATAGTG GAGGCAACTA TGACATGGCA AAACTTCTTA ATGGAACGGT TGTTCAAAAG 960

CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTA 1020

GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA 1080

CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA 1140

GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA 1200

CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG 1260

CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG 1320

TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA 1380

ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC 1440

ATTTGGGTGA AACGA 1455

(2) INFORMATION FOR SEQ ID NO: 11:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1548 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCACCGT TTAACGGCAC CATGATGCAG TATTTTGAAT GGTACTTGCC GGATGATGGC 60

ACGTTATGGA CCAAAGTGGC CAATGAAGCC AACAACTTAT CCAGCCTTGG CATCACCGCT 120

CTTTGGCTGC CGCCCGCTTA CAAAGGAACA AGCCGCAGCG ACGTAGGGTA CGGAGTATAC 180

GACTTGTATG ACCTCGGCGA ATTCAATCAA AAAGGGACCG TCCGCACAAA ATACGGAACA 240

AAAGCTCAAT ATCTTCAAGC CATTCAAGCC GCCCACGCCG CTGGAATGCA AGTGTACGCC 300

GATGTCGTGT TCGACCATAA AGGCGGCGCT GACGGCACGG AATGGGTGGA CGCCGTCGAA 360

GTCAATCCGT CCGACCGCAA CCAAGAAATC TCGGGCACCT ATCAAATCCA AGCATGGACG 420

AAATTTGATT TTCCCGGGCG GGGCAACACC TACTCCAGCT TTAAGTGGCG CTGGTACCAT 480

TTTGACGGCG TTGATTGGGA CGAAAGCCGA AAATTGAGCC GCATTTACAA ATTCCGCGGC 540

ATCGGCAAAG CGTGGGATTG GGAAGTAGAC ACGGAAAACG GAAACTATGA CTACTTAATG 600

TATGCCGACC TTGATATGGA TCATCCCGAA GTCGTGACCG AGCTGAAAAA CTGGGGGAAA 660

```
TGGTATGTCA ACACAACGAA CATTGATGGG TTCCGGCTTG ATGCCGTCAA GCATATTAAG     720
TTCAGTTTTT TTCCTGATTG GTTGTCGTAT GTGCGTTCTC AGACTGGCAA GCCGCTATTT     780
ACCGTCGGGG AATATTGGAG CTATGACATC AACAAGTTGC ACAATTACAT TACGAAAACA     840
GACGGAACGA TGTCTTTGTT TGATGCCCCG TTACACAACA AATTTTATAC CGCTTCCAAA     900
TCAGGGGGCG CATTTGATAT GCGCACGTTA ATGACCAATA CTCTCATGAA AGATCAACCG     960
ACATTGGCCG TCACCTTCGT TGATAATCAT GACACCGAAC CCGGCCAAGC GCTGCAGTCA    1020
TGGGTCGACC CATGGTTCAA ACCGTTGGCT TACGCCTTTA TTCTAACTCG GCAGGAAGGA    1080
TACCCGTGCG TCTTTTATGG TGACTATTAT GGCATTCCAC AATATAACAT TCCTTCGCTG    1140
AAAAGCAAAA TCGATCCGCT CCTCATCGCG CGCAGGGATT ATGCTTACGG AACGCAACAT    1200
GATTATCTTG ATCACTCCGA CATCATCGGG TGGACAAGGG AAGGGGGCAC TGAAAAACCA    1260
GGATCCGGAC TGGCCGCACT GATCACCGAT GGGCCGGGAG GAAGCAAATG GATGTACGTT    1320
GGCAAACAAC ACGCTGGAAA AGTGTTCTAT GACCTTACCG GCAACCGGAG TGACACCGTC    1380
ACCATCAACA GTGATGGATG GGGGGAATTC AAAGTCAATG GCGGTTCGGT TTCGGTTTGG    1440
GTTCCTAGAA AAACGACCGT TTCTACCATC GCTCGGCCGA TCACAACCCG ACCGTGGACT    1500
GGTGAATTCG TCCGTTGGAC CGAACCACGG TTGGTGGCAT GGCCTTGA                 1548
```

(2) INFORMATION FOR SEQ ID NO: 12:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1920 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION:421..1872
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
CGGAAGATTG GAAGTACAAA AATAAGCAAA AGATTGTCAA TCATGTCATG AGCCATGCGG      60
GAGACGGAAA AATCGTCTTA ATGCACGATA TTTATGCAAC GTTCGCAGAT GCTGCTGAAG     120
AGATTATTAA AAAGCTGAAA GCAAAAGGCT ATCAATTGGT AACTGTATCT CAGCTTGAAG     180
AAGTGAAGAA GCAGAGAGGC TATTGAATAA ATGAGTAGAA GCGCCATATC GGCGCTTTTC     240
TTTTGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT TTATACAACA     300
TCATATGTTT CACATTGAAA GGGGAGGAGA ATCATGAAAC AACAAAAACG GCTTTACGCC     360
```

CGATTGCTGA CGCTGTTATT TGCGCTCATC TTCTTGCTGC CTCATTCTGC AGCAGCGGCG 420

GCA AAT CTT AAT GGG ACG CTG ATG CAG TAT TTT GAA TGG TAC ATG CCC 468

AAT GAC GGC CAA CAT TGG AGG CGT TTG CAA AAC GAC TCG GCA TAT TTG 516

GCT GAA CAC GGT ATT ACT GCC GTC TGG ATT CCC CCG GCA TAT AAG GGA 564

ACG AGC CAA GCG GAT GTG GGC TAC GGT GCT TAC GAC CTT TAT GAT TTA 612

GGG GAG TTT CAT CAA AAA GGG ACG GTT CGG ACA AAG TAC GGC ACA AAA 660

GGA GAG CTG CAA TCT GCG ATC AAA AGT CTT CAT TCC CGC GAC ATT AAC 708

GTT TAC GGG GAT GTG GTC ATC AAC CAC AAA GGC GGC GCT GAT GCG ACC 756

GAA GAT GTA ACC GCG GTT GAA GTC GAT CCC GCT GAC CGC AAC CGC GTA 804

ATT TCA GGA GAA CAC CTA ATT AAA GCC TGG ACA CAT TTT CAT TTT CCG 852

GGG CGC GGC AGC ACA TAC AGC GAT TTT AAA TGG CAT TGG TAC CAT TTT 900

GAC GGA ACC GAT TGG GAC GAG TCC CGA AAG CTG AAC CGC ATC TAT AAG 948

TTT CAA GGA AAG GCT TGG GAT TGG GAA GTT TCC AAT GAA AAC GGC AAC 996

TAT GAT TAT TTG ATG TAT GCC GAC ATC GAT TAT GAC CAT CCT GAT GTC 1044

GCA GCA GAA ATT AAG AGA TGG GGC ACT TGG TAT GCC AAT GAA CTG CAA 1092

TTG GAC GGT TTC CGT CTT GAT GCT GTC AAA CAC ATT AAA TTT TCT TTT 1140

TTG CGG GAT TGG GTT AAT CAT GTC AGG GAA AAA ACG GGG AAG GAA ATG 1188

TTT ACG GTA GCT GAA TAT TGG CAG AAT GAC TTG GGC GCG CTG GAA AAC 1236

TAT TTG AAC AAA ACA AAT TTT AAT CAT TCA GTG TTT GAC GTG CCG CTT 1284

CAT TAT CAG TTC CAT GCT GCA TCG ACA CAG GGA GGC GGC TAT GAT ATG 1332

AGG AAA TTG CTG AAC GGT ACG GTC GTT TCC AAG CAT CCG TTG AAA TCG 1380

GTT ACA TTT GTC GAT AAC CAT GAT ACA CAG CCG GGG CAA TCG CTT GAG 1428

TCG ACT GTC CAA ACA TGG TTT AAG CCG CTT GCT TAC GCT TTT ATT CTC 1476

ACA AGG GAA TCT GGA TAC CCT CAG GTT TTC TAC GGG GAT ATG TAC GGG 1524

ACG AAA GGA GAC TCC CAG CGC GAA ATT CCT GCC TTG AAA CAC AAA ATT 1572

GAA CCG ATC TTA AAA GCG AGA AAA CAG TAT GCG TAC GGA GCA CAG CAT 1620

GAT TAT TTC GAC CAC CAT GAC ATT GTC GGC TGG ACA AGG GAA GGC GAC 1668

AGC TCG GTT GCA AAT TCA GGT TTG GCG GCA TTA ATA ACA GAC GGA CCC 1716

GGT GGG GCA AAG CGA ATG TAT GTC GGC CGG CAA AAC GCC GGT GAG ACA 1764

TGG CAT GAC ATT ACC GGA AAC CGT TCG GAG CCG GTT GTC ATC AAT TCG 1812

GAA GGC TGG GGA GAG TTT CAC GTA AAC GGC GGG TCG GTT TCA ATT TAT 1860

GTT CAA AGA TAG AAGAGCAGAG AGGACGGATT TCCTGAAGGA AATCCGTTTT 1912

TTTATTTT 1920

(2) INFORMATION FOR SEQ ID NO: 12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2084 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:343..1794
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCCCCGCACA TACGAAAAGA CTGGCTGAAA ACATTGAGCC TTTGATGACT GATGATTTGG 60

CTGAAGAAGT GGATCGATTG TTTGAGAAAA GAAGAAGACC ATAAAAATAC CTTGTCTGTC 120

ATCAGACAGG GTATTTTTTA TGCTGTCCAG ACTGTCCGCT GTGTAAAAAT AAGGAATAAA 180

GGGGGGTTGT TATTATTTTA CTGATATGTA AAATATAATT TGTATAAGAA AATGAGAGGG 240

AGAGGAAACA TGATTCAAAA ACGAAAGCGG ACAGTTTCGT TCAGACTTGT GCTTATGTGC 300

ACGCTGTTAT TTGTCAGTTT GCCGATTACA AAAACATCAG CC GTA AAT GGC ACG 354

CTG ATG CAG TAT TTT GAA TGG TAT ACG CCG AAC GAC GGC CAG CAT TGG 402

AAA CGA TTG CAG AAT GAT GCG GAA CAT TTA TCG GAT ATC GGA ATC ACT 450

GCC GTC TGG ATT CCT CCC GCA TAC AAA GGA TTG AGC CAA TCC GAT AAC 498

GGA TAC GGA CCT TAT GAT TTG TAT GAT TTA GGA GAA TTC CAG CAA AAA 546

GGG ACG GTC AGA ACG AAA TAC GGC ACA AAA TCA GAG CTT CAA GAT GCG 594

ATC GGC TCA CTG CAT TCC CGG AAC GTC CAA GTA TAC GGA GAT GTG GTT 642

TTG AAT CAT AAG GCT GGT GCT GAT GCA ACA GAA GAT GTA ACT GCC GTC 690

GAA GTC AAT CCG GCC AAT AGA AAT CAG GAA ACT TCG GAG GAA TAT CAA 738

ATC AAA GCG TGG ACG GAT TTT CGT TTT CCG GGC CGT GGA AAC ACG TAC 786

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AGT GAT TTT AAA TGG CAT TGG TAT CAT TTC GAC GGA GCG GAC TGG GAT      834
GAA TCC CGG AAG ATC AGC CGC ATC TTT AAG TTT CGT GGG GAA GGA AAA      882
GCG TGG GAT TGG GAA GTA TCA AGT GAA AAC GGC AAC TAT GAC TAT TTA      930
ATG TAT GCT GAT GTT GAC TAC GAC CAC CCT GAT GTC GTG GCA GAG ACA      978
AAA AAA TGG GGT ATC TGG TAT GCG AAT GAA CTG TCA TTA GAC GGC TTC     1026
CGT ATT GAT GCC GCC AAA CAT ATT AAA TTT TCA TTT CTG CGT GAT TGG     1074
GTT CAG GCG GTC AGA CAG GCG ACG GGA AAA GAA ATG TTT ACG GTT GCG     1122
GAG TAT TGG CAG AAT AAT GCC GGG AAA CTC GAA AAC TAC TTG AAT AAA     1170
ACA AGC TTT AAT CAA TCC GTG TTT GAT GTT CCG CTT CAT TTC AAT TTA     1218
CAG GCG GCT TCC TCA CAA GGA GGC GGA TAT GAT ATG AGG CGT TTG CTG     1266
GAC GGT ACC GTT GTG TCC AGG CAT CCG GAA AAG GCG GTT ACA TTT GTT     1314
GAA AAT CAT GAC ACA CAG CCG GGA CAG TCA TTG GAA TCG ACA GTC CAA     1362
ACT TGG TTT AAA CCG CTT GCA TAC GCC TTT ATT TTG ACA AGA GAA TCC     1410
GGT TAT CCT CAG GTG TTC TAT GGG GAT ATG TAC GGG ACA AAA GGG ACA     1458
TCG CCA AAG GAA ATT CCC TCA CTG AAA GAT AAT ATA GAG CCG ATT TTA     1506
AAA GCG CGT AAG GAG TAC GCA TAC GGG CCC CAG CAC GAT TAT ATT GAC     1554
CAC CCG GAT GTG ATC GGA TGG ACG AGG GAA GGT GAC AGC TCC GCC GCC     1602
AAA TCA GGT TTG GCC GCT TTA ATC ACG GAC GGA CCC GGC GGA TCA AAG     1650
CGG ATG TAT GCC GGC CTG AAA AAT GCC GGC GAG ACA TGG TAT GAC ATA     1698
ACG GGC AAC CGT TCA GAT ACT GTA AAA ATC GGA TCT GAC GGC TGG GGA     1746
GAG TTT CAT GTA AAC GAT GGG TCC GTC TCC ATT TAT GTT CAG AAA TAA     1794
GGTAATAAAA AAACACCTCC AAGCTGAGTG CGGGTATCAG CTTGGAGGTG CGTTTATTTT   1854
TTCAGCCGTA TGACAAGGTC GGCATCAGGT GTGACAAATA CGGTATGCTG GCTGTCATAG   1914
GTGACAAATC CGGGTTTTGC GCCGTTTGGC TTTTTCACAT GTCTGATTTT TGTATAATCA   1974
ACAGGCACGG AGCCGGAATC TTTCGCCTTG GAAAAATAAG CGGCGATCGT AGCTGCTTCC   2034
AATATGGATT GTTCATCGGG ATCGCTGCTT TTAATCACAA CGTGGGATCC              2084
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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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CATCATAATG GAACAAATGG TACTATGATG CAATATTTCG AATGGTATTT GCCAAATGAC     60
GGGAATCATT GGAACAGGTT GAGGGATGAC GCAGCTAACT TAAAGAGTAA AGGGATAACA    120
GCTGTATGGA TCCCACCTGC ATGGAAGGGG ACTTCCCAGA ATGATGTAGG TTATGGAGCC    180
TATGATTTAT ATGATCTTGG AGAGTTTAAC CAGAAGGGGA CGGTTCGTAC AAAATATGGA    240
ACACGCAACC AGCTACAGGC TGCGGTGACC TCTTTAAAAA ATAACGGCAT TCAGGTATAT    300
GGTGATGTCG TCATGAATCA TAAAGGTGGA GCAGATGGTA CGGAAATTGT AAATGCGGTA    360
GAAGTGAATC GGAGCAACCG AAACCAGGAA ACCTCAGGAG AGTATGCAAT AGAAGCGTGG    420
ACAAAGTTTG ATTTTCCTGG AAGAGGAAAT AACCATTCCA GCTTTAAGTG GCGCTGGTAT    480
CATTTTGATG GGACAGATTG GGATCAGTCA CGCCAGCTTC AAAACAAAAT ATATAAATTC    540
AGGGGAACAG GCAAGGCCTG GGACTGGGAA GTCGATACAG AGAATGGCAA CTATGACTAT    600
CTTATGTATG CAGACGTGGA TATGGATCAC CCAGAAGTAA TACATGAACT TAGAAACTGG    660
GGAGTGTGGT ATACGAATAC ACTGAACCTT GATGGATTTA GAATAGATGC AGTGAAACAT    720
ATAAAATATA GCTTTACGAG AGATTGGCTT ACACATGTGC GTAACACCAC AGGTAAACCA    780
ATGTTTGCAG TGGCTGAGTT TTGGAAAAAT GACCTTGGTG CAATTGAAAA CTATTTGAAT    840
AAAACAAGTT GGAATCACTC GGTGTTTGAT GTTCCTCTCC ACTATAATTT GTACAATGCA    900
TCTAATAGCG GTGGTTATTA TGATATGAGA AATATTTTAA ATGGTTCTGT GGTGCAAAAA    960
CATCCAACAC ATGCCGTTAC TTTTGTTGAT AACCATGATT CTCAGCCCGG GGAAGCATTG   1020
GAATCCTTTG TTCAACAATG GTTTAAACCA CTTGCATATG CATTGGTTCT GACAAGGGAA   1080
CAAGGTTATC CTTCCGTATT TTATGGGGAT TACTACGGTA TCCCAACCCA TGGTGTTCCG   1140
GCTATGAAAT CTAAAATAGA CCCTCTTCTG CAGGCACGTC AAACTTTTGC CTATGGTACG   1200
CAGCATGATT ACTTTGATCA TCATGATATT ATCGGTTGGA CAAGAGAGGG AAATAGCTCC   1260
CATCCAAATT CAGGCCTTGC CACCATTATG TCAGATGGTC CAGGTGGTAA CAAATGGATG   1320
TATGTGGGGA AAAATAAAGC GGGACAAGTT TGGAGAGATA TTACCGGAAA TAGGACAGGC   1380
ACCGTCACAA TTAATGCAGA CGGATGGGGT AATTTCTCTG TTAATGGAGG GTCCGTTTCG   1440
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GTTTGGGTGA AGCAA 1455

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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CATCATAATG GGACAAATGG GACGATGATG CAATACTTTG AATGGCACTT GCCTAATGAT      60
GGGAATCACT GGAATAGATT AAGAGATGAT GCTAGTAATC TAAGAAATAG AGGTATAACC     120
GCTATTTGGA TTCCGCCTGC CTGGAAAGGG ACTTCGCAAA ATGATGTGGG GTATGGAGCC     180
TATGATCTTT ATGATTTAGG GGAATTTAAT CAAAAGGGGA CGGTTCGTAC TAAGTATGGG     240
ACACGTAGTC AATTGGAGTC TGCCATCCAT GCTTTAAAGA ATAATGGCGT TCAAGTTTAT     300
GGGGATGTAG TGATGAACCA TAAAGGAGGA GCTGATGCTA CAGAAAACGT TCTTGCTGTC     360
GAGGTGAATC CAAATAACCG GAATCAAGAA ATATCTGGGG ACTACACAAT TGAGGCTTGG     420
ACTAAGTTTG ATTTTCCAGG GAGGGGTAAT ACATACTCAG ACTTTAAATG GCGTTGGTAT     480
CATTTCGATG GTGTAGATTG GGATCAATCA CGACAATTCC AAAATCGTAT CTACAAATTC     540
CGAGGTGATG GTAAGGCATG GGATTGGGAA GTAGATTCGG AAAATGGAAA TTATGATTAT     600
TTAATGTATG CAGATGTAGA TATGGATCAT CCGGAGGTAG TAAATGAGCT TAGAAGATGG     660
GGAGAATGGT ATACAAATAC ATTAAATCTT GATGGATTTA GGATCGATGC GGTGAAGCAT     720
ATTAAATATA GCTTTACACG TGATTGGTTG ACCCATGTAA GAAACGCAAC GGGAAAAGAA     780
ATGTTTGCTG TTGCTGAATT TTGGAAAAAT GATTTAGGTG CCTTGGAGAA CTATTTAAAT     840
AAAACAAACT GGAATCATTC TGTCTTTGAT GTCCCCCTTC ATTATAATCT TTATAACGCG     900
TCAAATAGTG GAGGCAACTA TGACATGGCA AAACTTCTTA ATGGAACGGT TGTTCAAAAG     960
CATCCAATGC ATGCCGTAAC TTTTGTGGAT AATCACGATT CTCAACCTGG GGAATCATTA    1020
GAATCATTTG TACAAGAATG GTTTAAGCCA CTTGCTTATG CGCTTATTTT AACAAGAGAA    1080
CAAGGCTATC CCTCTGTCTT CTATGGTGAC TACTATGGAA TTCCAACACA TAGTGTCCCA    1140
GCAATGAAAG CCAAGATTGA TCCAATCTTA GAGGCGCGTC AAAATTTTGC ATATGGAACA    1200
CAACATGATT ATTTTGACCA TCATAATATA ATCGGATGGA CACGTGAAGG AAATACCACG    1260
CATCCCAATT CAGGACTTGC GACTATCATG TCGGATGGGC CAGGGGGAGA GAAATGGATG    1320
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TACGTAGGGC AAAATAAAGC AGGTCAAGTT TGGCATGACA TAACTGGAAA TAAACCAGGA 1380

ACAGTTACGA TCAATGCAGA TGGATGGGCT AATTTTTCAG TAAATGGAGG ATCTGTTTCC 1440

ATTTGGGTGA AACGA 1455

(2) INFORMATION FOR SEQ ID NO: 15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSG1"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCATGATGCA GTATTTTGAA TGG

13

(2) INFORMATION FOR SEQ ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSG3"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GTCACCATAA AAGACGCACG GG

12

(2) INFORMATION FOR SEQ ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSGM1"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTCATAGTTT CCGAATTCCG TGTCTACTTC CCAATCCCAA TCCCAAGCTT

TGCCGCGGAA TTTGTAAATG

70

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSGM2"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTACTTCCCA ATCCCAAGCT TTGCCGCGGA ATTTGTAAAT G 41

(2) INFORMATION FOR SEQ ID NO: 19:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSGM3"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGATGATCCA TGTCAAAGTCG GCATAC

26

(2) INFORMATION FOR SEQ ID NO: 20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSGM4"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTCGGTCACC ACGTGGGGAT GATCC

25

(2) INFORMATION FOR SEQ ID NO: 21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer BSGM5"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCAGTTTTTC AGCTGGGTCA CGAC 24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 98/00444

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12N 9/28, C11D 3/386

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12N, C11D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, PAJ, BIOSIS, CA

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 9741213 A1 (NOVO NORDISK A/S), 6 November 1997 (06.11.97), page 15, line 23 - page 17, line 4 --	1-33
X	WO 9623873 A1 (NOVO NORDISK A/S), 8 August 1996 (08.08.96), page 21 - page 38; page 75 - page 77 --	1-33
X	WO 9510603 A1 (NOVO NORDISK A/S), 20 April 1995 (20.04.95), page 18, line 1 - page 20, line 14 --	1-33
A	WO 9535382 A2 (GIST-BROCADES B.V.), 28 December 1995 (28.12.95), page 3, line 20 - line 26, claims --	1-33

[X] Further documents are listed in the continuation of Box C. [X] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" erlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
20 January 1999	25 -01- 1999
Name and mailing address of the ISA/ Swedish Patent Office Box 5055, S-102 42 STOCKHOLM Facsimile No. +46 8 666 02 86	Authorized officer Yvonne Siösteen Telephone No. +46 8 782 25 00

International application No.
PCT/DK 98/00444

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 9100353 A2 (GIST-BROCADES N.V.), 10 January 1991 (10.01.91) --	1-33

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 98/00444

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [ ] Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. [ ] Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. [ ] Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The claimed inventions relates to variants of a parent Termamyl-like alpha-amylase. A large number of combinations of mutations are suggested, which give increased thermostability at acid pH and/or low Ca2+ concentrations.
Several different combinations of mutations of α-amylases giving more thermostable enzyms are well-known in the art, see search report. As no common theory for all the mutations are suggested in the present application no "special technical feature" that makes a contribution to the prior art, as demanded in PCT rule 13.2 has been found. Although the application claims a large number of inventions all of them have been searched.

1. [ ] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. [X] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest [ ] The additional search fees were accompanied by the applicant's protest.
[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT
Information on patent family members

01/12/98

International application No.
PCT/DK 98/00444

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9741213 A1	06/11/97	AU 2692897 A	19/11/97
WO 9623873 A1	08/08/96	AU 4483396 A	21/08/96
		BR 9607735 A	14/07/98
		CA 2211405 A	08/08/96
		CN 1172500 A	04/02/98
		EP 0815208 A	07/01/98
WO 9510603 A1	20/04/95	AU 7807494 A	04/05/95
		BR 9407767 A	18/03/97
		CA 2173329 A	20/04/95
		CN 1134725 A	30/10/96
		EP 0722490 A	24/07/96
		FI 961524 A	30/05/96
		JP 9503916 T	22/04/97
		US 5753460 A	19/05/98
		US 5801043 A	01/09/98
WO 9535382 A2	28/12/95	AU 685638 B	22/01/98
		AU 2524795 A	15/01/96
		EP 0772684 A	14/05/97
WO 9100353 A2	10/01/91	AT 166922 T	15/06/98
		AU 638263 B	24/06/93
		AU 5953890 A	17/01/91
		BG 61081 B	31/10/96
		CA 2030554 A	30/12/90
		CN 1050220 A	27/03/91
		DE 69032360 D	00/00/00
		EP 0410498 A,B	30/01/91
		SE 0410498 T3	
		ES 2117625 T	16/08/98
		FI 910907 D	00/00/00
		JP 4500756 T	13/02/92
		PT 94560 A,B	08/02/91
		US 5364782 A	15/11/94